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# Genetically-Engineered Amino Acid Substitutions in the Carboxy-Terminal End of Threonine Dehydratase/Deaminase of *Arabidopsis thaliana* Reveal a Synergistic Interaction Between Two Different Effector-Binding Sites

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We fused four mutant *omr1* alleles, encoding feedback-insensitive forms of *Arabidopsis thaliana* biosynthetic threonine dehydratase/deaminase (TD), to the CaMV 35S promoter and transformed these constructs into *A. thaliana* Columbia wild type plants. The mutant TD forms consisted of our previously isolated double mutant, *omr1-1*, and three new site-directed mutants, *omr1-5*, *omr1-7*, and *omr1-8* with single point mutations. We employed site-directed mutagenesis to assay the effects of amino acid substitutions in separate regulatory regions within the carboxy-terminal (C-term) allosteric end. TD assays and growth resistance to the isoleucine (Ile) toxic analog L-O-methylthreonine (OMT) confirmed the desensitization to feedback inhibition and the viability of these mutant *omr1* alleles as selectable markers, respectively. Two of the site-directed mutants, *omr1-5* and *omr1-7*, appeared to influence one of the two separate Ile-binding sites and had a notable 13-fold and 15-fold increase in free Ile, respectively. The *omr1-8* appeared to influence the other Ile-binding site and resulted in a 2-fold increase in free Ile. The transgenic *omr1-1* double mutant affecting both Ile-binding sites, however, displayed a 106-fold increase in free Ile revealing a profound synergistic interplay between these separate Ile-binding sites.